

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Reed, Guy  
Clement, Christophe Y.
- (ii) TITLE OF THE INVENTION: NOVEL PLATELET ACTIVATION PROTEIN
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Fish & Richardson P.C.
  - (B) STREET: 225 Franklin Street
  - (C) CITY: Boston
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 04-OCT-1996
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 60/005,074
  - (B) FILING DATE: 06-OCT-1995
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Fraser, Janis K
  - (B) REGISTRATION NUMBER: 34,819
  - (C) REFERENCE/DOCKET NUMBER: 05433/020001
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 617-542-5070
  - (B) TELEFAX: 617-542-8906
  - (C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1373 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 44...1321
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGAGAGGGC CAGAGGAGAA AGAGAGAGCG CGAAAGAGAG AGG	ATG TCT CTC TCA	55
	Met Ser Leu Ser	
	1	
GAC TGG CAC CTG GCG GTG AAG CTG GCT GAC CAG CCA CTT ACT CCA AAG		103
Asp Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro Leu Thr Pro Lys		
5	10	20
TCT ATT CTT CGG TTG CCA GAG ACA GAA CTG GGA GAA TAC TCG CTA GGG		151
Ser Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu Tyr Ser Leu Gly		
	25	30
		35
GGC TAT AGT ATT TCA TTT CTG AAG CAG CTT ATT GCT GGC AAA CTC CAG		199
Gly Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala Gly Lys Leu Gln		
	40	45
		50
GAG TCT GTT CCA GAC CCT GAG CTG ATT GAT CTG ATC TAC TGT GGT CGG		247
Glu Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile Tyr Cys Gly Arg		
	55	60
		65
AAG CTA AAA GAT GAC CAG ACA CTT GAC TTC TAT GGC ATT CAA CCT GGG		295
Lys Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly Ile Gln Pro Gly		
	70	75
		80
TCC ACT GTC CAT GTT CTG CGA AAG TCC TGG CCT GAA CCT GAT CAG AAA		343
Ser Thr Val His Val Leu Arg Lys Ser Trp Pro Glu Pro Asp Gln Lys		
85	90	100
CCG GAA CCT GTG GAC AAA GTG GCT GCC ATG AGA GAG TTC CGG GTG TTG		391
Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu Phe Arg Val Leu		
	105	110
		115
CAC ACT GCC CTG CAC AGC AGC TCC TCT TAC AGG GAG GCG GTC TTT AAG		439
His Thr Ala Leu His Ser Ser Ser Ser Tyr Arg Glu Ala Val Phe Lys		
	120	125
		130
ATG CTC AGC AAT AAG GAG TCT CTG GAT CAG ATC ATT GTG GCC ACC CCA		487
Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile Val Ala Thr Pro		
	135	140
		145
GGC CTC AGC AGT GAC CCT ATT GCT CTT GGG GTT CTC CAG GAC AAG GAC		535
Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu Gln Asp Lys Asp		
	150	155
		160
CTC TTC TCT GTC TTC GCT GAT CCC AAT ATG CTT GAT ACG TTG GTG CCT		583
Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp Thr Leu Val Pro		
165	170	175
		180

GCT CAC CCA GCC CTC GTC AAT GCC ATT GTC CTG GTT CTG CAC TCC GTA	631
Ala His Pro Ala Leu Val Asn Ala Ile Val Leu Val Leu His Ser Val	
185 190 195	
GCA GGC AGT GCC CCA ATG CCT GGG ACT GAC TCC TCT TCC CGG AGC ATG	679
Ala Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser Ser Arg Ser Met	
200 205 210	
CCC TCC AGC TCA TAC CGG GAT ATG CCA GGT GGC TTC CTG TTT GAA GGG	727
Pro Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe Leu Phe Glu Gly	
215 220 225	
CTC TCA GAT GAT GAG GAT GAC TTT CAC CCA AAC ACC AGG TCC ACA CCC	775
Leu Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr Arg Ser Thr Pro	
230 235 240	
TCT AGC AGT ACT CCC AGC TCC CGC CCA GCC TCC CTG GGG TAC AGT GGA	823
Ser Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu Gly Tyr Ser Gly	
245 250 255 260	
GCT GCT GGG CCC CGG CCC ATC ACC CAG AGT GAG CTG GCC ACC GCC TTG	871
Ala Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu Ala Thr Ala Leu	
265 270 275	
GCC CTG GCC AGC ACT CCG GAG AGC AGC TCT CAC ACA CCG ACT CCT GGC	919
Ala Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr Pro Thr Pro Gly	
280 285 290	
ACC CAG GGT CAT TCC TCA GGG ACC TCA CCA ATG TCC TCT GGT GTC CAG	967
Thr Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser Ser Gly Val Gln	
295 300 305	
TCA GGG ACG CCC ATC ACC AAT GAT CTC TTC AGC CAA GCC CTA CAG CAT	1015
Ser Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln Ala Leu Gln His	
310 315 320	
GCC CTT CAG GCC TCT GGG CAG CCC AGC CTT CAG AGC CAG TGG CAG CCC	1063
Ala Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser Gln Trp Gln Pro	
325 330 335 340	
CAG CTG CAG CAG CTA CGT GAC ATG GGC ATC CAG GAC GAT GAG CTG AGC	1111
Gln Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp Asp Glu Leu Ser	
345 350 355	
CTG CGG CCC TGC AGG CCA CCG GTG GGG ACA TCC AAG CAG CCC TGG AGC	1159
Leu Arg Pro Cys Arg Pro Pro Val Gly Thr Ser Lys Gln Pro Trp Ser	
360 365 370	
TCA TCT TTG CTG GAG GAG CCC CAT GAA CTC CCT GCT TCC CCT GAA CCC	1207
Ser Ser Leu Leu Glu Glu Pro His Glu Leu Pro Ala Ser Pro Glu Pro	
375 380 385	
CCA GCA AGT TGC AGA GGC TAC TGC CCT TGG GAG GCA CTC ATG AAG GTG	1255
Pro Ala Ser Cys Arg Gly Tyr Cys Pro Trp Glu Ala Leu Met Lys Val	
390 395 400	



Ala	Thr	Ala	Leu	Ala	Leu	Ala	Ser	Thr	Pro	Glu	Ser	Ser	Ser	His	Thr
	275						280					285			
Pro	Thr	Pro	Gly	Thr	Gln	Gly	His	Ser	Ser	Gly	Thr	Ser	Pro	Met	Ser
	290						295				300				
Ser	Gly	Val	Gln	Ser	Gly	Thr	Pro	Ile	Thr	Asn	Asp	Leu	Phe	Ser	Gln
	305				310					315					320
Ala	Leu	Gln	His	Ala	Leu	Gln	Ala	Ser	Gly	Gln	Pro	Ser	Leu	Gln	Ser
			325						330					335	
Gln	Trp	Gln	Pro	Gln	Leu	Gln	Gln	Leu	Arg	Asp	Met	Gly	Ile	Gln	Asp
		340					345						350		
Asp	Glu	Leu	Ser	Leu	Arg	Pro	Cys	Arg	Pro	Pro	Val	Gly	Thr	Ser	Lys
	355						360					365			
Gln	Pro	Trp	Ser	Ser	Ser	Leu	Leu	Glu	Glu	Pro	His	Glu	Leu	Pro	Ala
	370					375					380				
Ser	Pro	Glu	Pro	Pro	Ala	Ser	Cys	Arg	Gly	Tyr	Cys	Pro	Trp	Glu	Ala
	385				390					395					400
Leu	Met	Lys	Val	Pro	Pro	Ser	Leu	Pro	Ser	Pro	Ile	Tyr	Leu	Met	Val
			405						410					415	
Asn	Ser	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys						
		420					425								

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 44...1273
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGAGAGGGC	CAGAGGAGAA	AGAGAGAGCG	CGAAAGAGAG	AGG	ATG	TCT	CTC	TCA		55
					Met	Ser	Leu	Ser		
					1					
GAC TGC	CAC CTG	GCG GTG	AAG CTG	GCT GAC	CAG CCA	CTT ACT	CCA AAG		103	
Asp Trp	His Leu	Ala Val	Lys Leu	Ala Asp	Gln Pro	Leu Thr	Pro Lys			
5		10		15			20			
TCT ATT	CTT CGG	TTG CCA	GAG ACA	GAA CTG	GGA GAA	TAC TCG	CTA GGG		151	
Ser Ile	Leu Arg	Leu Pro	Glu Thr	Glu Leu	Gly Glu	Tyr Ser	Leu Gly			
	25			30			35			
GGC TAT	AGT ATT	TCA TTT	CTG AAG	CAG CTT	ATT GCT	GGC AAA	CTC CAG		199	
Gly Tyr	Ser Ile	Ser Phe	Leu Lys	Gln Leu	Ile Ala	Gly Lys	Leu Gln			
	40			45		50				
GAG TCT	GTT CCA	GAC CCT	GAG CTG	ATT GAT	CTG ATC	TAC TGT	GGT CGG		247	
Glu Ser	Val Pro	Asp Pro	Glu Leu	Ile Asp	Leu Ile	Tyr Cys	Gly Arg			
	55		60			65				

AAG CTA AAA GAT GAC CAG ACA CTT GAC TTC TAT GGC ATT CAA CCT GGG Lys Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly Ile Gln Pro Gly 70 75 80	295
TCC ACT GTC CAT GTT CTG CGA AAG TCC TGG CCT GAA CCT GAT CAG AAA Ser Thr Val His Val Leu Arg Lys Ser Trp Pro Glu Pro Asp Gln Lys 85 90 95 100	343
CCG GAA CCT GTG GAC AAA GTG GCT GCC ATG AGA GAG TTC CGG GTG TTG Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu Phe Arg Val Leu 105 110 115	391
CAC ACT GCC CTG CAC AGC AGC TCC TCT TAC AGG GAG GCG GTC TTT AAG His Thr Ala Leu His Ser Ser Ser Ser Tyr Arg Glu Ala Val Phe Lys 120 125 130	439
ATG CTC AGC AAT AAG GAG TCT CTG GAT CAG ATC ATT GTG GCC ACC CCA Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile Val Ala Thr Pro 135 140 145	487
GGC CTC AGC AGT GAC CCT ATT GCT CTT GGG GTT CTC CAG GAC AAG GAC Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu Gln Asp Lys Asp 150 155 160	535
CTC TTC TCT GTC TTC GCT GAT CCC AAT ATG CTT GAT ACG TTG GTG CCT Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp Thr Leu Val Pro 165 170 175 180	583
GCT CAC CCA GCC CTC GTC AAT GCC ATT GTC CTG GTT CTG CAC TCC GTA Ala His Pro Ala Leu Val Asn Ala Ile Val Leu Val Leu His Ser Val 185 190 195	631
GCA GGC AGT GCC CCA ATG CCT GGG ACT GAC TCC TCT TCC CGG AGC ATG Ala Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser Ser Arg Ser Met 200 205 210	679
CCC TCC AGC TCA TAC CGG GAT ATG CCA GGT GGC TTC CTG TTT GAA GGG Pro Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe Leu Phe Glu Gly 215 220 225	727
CTC TCA GAT GAT GAG GAT GAC TTT CAC CCA AAC ACC AGG TCC ACA CCC Leu Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr Arg Ser Thr Pro 230 235 240	775
TCT AGC AGT ACT CCC AGC TCC CGC CCA GCC TCC CTG GGG TAC AGT GGA Ser Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu Gly Tyr Ser Gly 245 250 255 260	823
GCT GCT GGG CCC CGG CCC ATC ACC CAG AGT GAG CTG GCC ACC GCC TTG Ala Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu Ala Thr Ala Leu 265 270 275	871
GCC CTG GCC AGC ACT CCG GAG AGC AGC TCT CAC ACA CCG ACT CCT GGC Ala Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr Pro Thr Pro Gly 280 285 290	919

ACC CAG GGT CAT TCC TCA GGG ACC TCA CCA ATG TCC TCT GGT GTC CAG	967
Thr Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser Ser Gly Val Gln	
295 300 305	
TCA GGG ACG CCC ATC ACC AAT GAT CTC TTC AGC CAA GCC CTA CAG CAT	1015
Ser Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln Ala Leu Gln His	
310 315 320	
GCC CTT CAG GCC TCT GGG CAG CCC AGC CTT CAG AGC CAG TGG CAG CCC	1063
Ala Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser Gln Trp Gln Pro	
325 330 335 340	
CAG CTG CAG CAG CTA CGT GAC ATG GGC ATC CAG GAC GAT GAG CTG AGC	1111
Gln Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp Asp Glu Leu Ser	
345 350 355	
CTG CGG CCC TGC AGG CCA CCG GTG GGG ACA TCC AAG CAG CCC TGG AGC	1159
Leu Arg Pro Cys Arg Pro Pro Val Gly Thr Ser Lys Gln Pro Trp Ser	
360 365 370	
TCA TCT TTG CTG GAG GAG CCC CAT GAA CTC CCT GCT TCC CCT GAA CCC	1207
Ser Ser Leu Leu Glu Glu Pro His Glu Leu Pro Ala Ser Pro Glu Pro	
375 380 385	
CCA GCA AGT TGC AGA GGC TAC TGC CCT TGG GAG GCA CTC ATG AAG GTG	1255
Pro Ala Ser Cys Arg Gly Tyr Cys Pro Trp Glu Ala Leu Met Lys Val	
390 395 400	
CCT CCA TCT CTC CCT GTC	
1273	
Pro Pro Ser Leu Pro Val	
405 410	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Leu	Ser	Asp	Trp	His	Leu	Ala	Val	Lys	Leu	Ala	Asp	Gln	Pro
1				5					10					15	
Leu	Thr	Pro	Lys	Ser	Ile	Leu	Arg	Leu	Pro	Glu	Thr	Glu	Leu	Gly	Glu
			20					25					30		
Tyr	Ser	Leu	Gly	Gly	Tyr	Ser	Ile	Ser	Phe	Leu	Lys	Gln	Leu	Ile	Ala
			35				40					45			
Gly	Lys	Leu	Gln	Glu	Ser	Val	Pro	Asp	Pro	Glu	Leu	Ile	Asp	Leu	Ile
			50			55				60					
Tyr	Cys	Gly	Arg	Lys	Leu	Lys	Asp	Asp	Gln	Thr	Leu	Asp	Phe	Tyr	Gly
65					70					75					80

Ile	Gln	Pro	Gly	Ser	Thr	Val	His	Val	Leu	Arg	Lys	Ser	Trp	Pro	Glu		
				85					90					95			
Pro	Asp	Gln	Lys	Pro	Glu	Pro	Val	Asp	Lys	Val	Ala	Ala	Met	Arg	Glu		
			100					105					110				
Phe	Arg	Val	Leu	His	Thr	Ala	Leu	His	Ser	Ser	Ser	Ser	Tyr	Arg	Glu		
			115					120					125				
Ala	Val	Phe	Lys	Met	Leu	Ser	Asn	Lys	Glu	Ser	Leu	Asp	Gln	Ile	Ile		
			130					135				140					
Val	Ala	Thr	Pro	Gly	Leu	Ser	Ser	Asp	Pro	Ile	Ala	Leu	Gly	Val	Leu		
					150					155					160		
Gln	Asp	Lys	Asp	Leu	Phe	Ser	Val	Phe	Ala	Asp	Pro	Asn	Met	Leu	Asp		
				165						170				175			
Thr	Leu	Val	Pro	Ala	His	Pro	Ala	Leu	Val	Asn	Ala	Ile	Val	Leu	Val		
				180						185				190			
Leu	His	Ser	Val	Ala	Gly	Ser	Ala	Pro	Met	Pro	Gly	Thr	Asp	Ser	Ser		
			195					200					205				
Ser	Arg	Ser	Met	Pro	Ser	Ser	Ser	Tyr	Arg	Asp	Met	Pro	Gly	Gly	Phe		
			210					215				220					
Leu	Phe	Glu	Gly	Leu	Ser	Asp	Asp	Glu	Asp	Asp	Phe	His	Pro	Asn	Thr		
					230					235					240		
Arg	Ser	Thr	Pro	Ser	Ser	Ser	Thr	Pro	Ser	Ser	Arg	Pro	Ala	Ser	Leu		
				245						250					255		
Gly	Tyr	Ser	Gly	Ala	Ala	Gly	Pro	Arg	Pro	Ile	Thr	Gln	Ser	Glu	Leu		
			260					265					270				
Ala	Thr	Ala	Leu	Ala	Leu	Ala	Ser	Thr	Pro	Glu	Ser	Ser	Ser	His	Thr		
			275					280					285				
Pro	Thr	Pro	Gly	Thr	Gln	Gly	His	Ser	Ser	Gly	Thr	Ser	Pro	Met	Ser		
			290					295				300					
Ser	Gly	Val	Gln	Ser	Gly	Thr	Pro	Ile	Thr	Asn	Asp	Leu	Phe	Ser	Gln		
				310						315					320		
Ala	Leu	Gln	His	Ala	Leu	Gln	Ala	Ser	Gly	Gln	Pro	Ser	Leu	Gln	Ser		
				325						330					335		
Gln	Trp	Gln	Pro	Gln	Leu	Gln	Gln	Leu	Arg	Asp	Met	Gly	Ile	Gln	Asp		
			340						345				350				
Asp	Glu	Leu	Ser	Leu	Arg	Pro	Cys	Arg	Pro	Pro	Val	Gly	Thr	Ser	Lys		
			355					360				365					
Gln	Pro	Trp	Ser	Ser	Ser	Leu	Glu	Glu	Pro	His	Glu	Leu	Pro	Ala			
			370					375				380					
Ser	Pro	Glu	Pro	Pro	Ala	Ser	Cys	Arg	Gly	Tyr	Cys	Pro	Trp	Glu	Ala		
				385				390			395				400		
Leu	Met	Lys	Val	Pro	Pro	Ser	Leu	Pro	Val								
				405					410								

We claim: